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KSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQT
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ORGANISM: Homo sapiens
       US-09-789-300A-2
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LENGTH: 340
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14107, A
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22707, Ap
12639, Ap
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3648, Ap
1046, Ap
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2928, Ap
3878, Ap
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                                             April 22, 2005, 16:19:29 ; Search time 29.9558 Seconds (without alignments) 844.779 Million cell updates/sec
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1 MCAQYCISFADVEKAHINIQ......TSLNWVGQAERPAPYQTVSV 339
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Sequence 5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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| S-09-252-991A-31294
| S-09-489-093A-14107
| S-09-328-352-5207
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| S-09-134-001C-3876
| S-09-134-001C-3876
| S-09-134-001C-3876
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-09-328-352-4536
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1075, Ap
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25027, A
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APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR PILING DATE: 2000-02-17
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Query Match 90.9%; Score 1582.5; DB 4; Best Local Similarity 89.7%; Pred. No. 1.6e-165; Matches 305; Conservative 19; Mismatches 15;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 31294, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABOUT STAND AND AND AND AND AND AND THERAPEUTICS
TITLE OF INVENTION: ABOUT STAND STAND AND AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
                                                  68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                         187
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31.2%; Score 543; DB 4; Le
Best Local Similarity 38.7%; Pred. No. 6.9e-51;
Matches 121; Conservative 63; Mismatches 121;
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US-09-252-991A-31294
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353 RVGILLSGGNIDL 365
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US-09-252-991A-31294
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                                Sequence 4645, Application US/09543681A
Patent No. 6605709
Patent No. 6605709
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4645
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Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-0.54

SEQ ID NO. 5EQ ID NOS: 8252
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LENGREN: 328
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Pred. No. 6.5e-58;
9; Mismatches 108; Indels
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Best Local Similarity 40.8%; Pred. No. 2.7e-54;
Matches 129; Conservative 62; Mismatches 113; Indels
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Best Local Similarity 40.9%; Pre
Matches 128; Conservative 69;
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                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Proteus mirabilis
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310 KIGIIISGGNVDI 322
                   US-09-543-681A-4645
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US-09-328-352-4536
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ORGANISM: Acinetobacter baumannii
US-09-328-352-5207
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Best Local Similarity 37.7%;
Matches 116; Conservative 5
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US-09-328-352-5207
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FACEDIAN NO. 6551795
GENERAL INFORMATION:
FACEDIAN MACHINE MACHINE MACHINE AND MAINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBRUE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27783
                                                                     Sequence 14107, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BREAD et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 L---TAAEKRKGVVACSAGNHAQGVSLSCAMLGIDGKVVMPKGAPKSKVAATCDYSAEVV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 -YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 LHGDNFNDTLAKASDIV--ELEGRIFIPPYDDPQVIAGGGTIGLEILEDLYDVDNVIVPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 PGKLTYEIARQLVDDIVLVSEDDIRQSMVALIQRNKVITEGAGALACAALLSGKLDSYIQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 IGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VSIDDILEAKQRLAGKIYKTGMPRSNYFSERCQGEIFLKFENMQRTGSFKIRGAFNKLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 27.6%; Score 480; DB 4;
Best Local Similarity 36.3%; Pred. No. 5e-44;
Matches 117; Conservative 66; Mismatches 129,
                                                                                                                                                                                        FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOO 14107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 EVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 NRKTVSLI-SGGNIDLSRVSQI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14107
                                                         US-09-489-039A-14107
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Sequence 2207, Application US/09328352

Patent No. 6562958
GRNERAL INFORMATION:
APPLICAMY: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown US-09-252-991A-27783
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                                                                                                                                                                                                                                                                                                                                                                       98 NHAQGLALAAAXRQGIRAVIVMPKTTPEIKVQAVRAHGAKAVLHGDAFPEALAHAL-KLVD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 TEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AGIAITIKALKPSVKVYAAE----PSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ETEGILVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGWVAGIAITIKALKPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 TPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 SDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                          41 TPLQPARQLSERLGNQVLLKREDLQPVFSFKIRGAYNKVAQL---TEEEKARGVIAASAG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 VKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRDLVDDVFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 TPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSG
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us-09-889-609b-8.rai

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PARCEL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                        66 GLIPDIPEEKPKAVVTHSSGNHGQALIYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA-S 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 VK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 VAVKRIGDETFRLCQKYVDDVITVDSDAICAAVKDLFEDVRAIAEPSGALALAG-LKKYV 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SFADVEKAHIN--IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIR
                                                                                                                                                                                                                                                           13 SSAEYLKAALSAPVYEAAVVTPLQEMAKISQRLENTILVKREDRQPVHSFKLRGAYNMIA
                                                                                                                                                                                                                                                                                                                                                                                             125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV
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                                                                                                                                                                   66; Mismatches 130; Indels
                                                                                                                        Score 418; DB 4;
Pred. No. 7.3e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 QTVSPEVKNVCIVLSGGNVDLTSLNWVGQ 327
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                                                                                                               24.0%;
34.3%;
                                                    ; ORGANISM: Proteus mirabilis US-09-543-681A-4364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22442
                                                                                                                                                                   Matches 113; Conservative
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                                                                                                                                              Best Local Similarity
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US-09-252-991A-22442
         LENGTH: 525
TYPE: PRT
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                                                                                                                        Query Match
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GRNERAL INFORMATION:
APPLICANT GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
ELTIQIAKHFVDDIVVVTEDMIEEAIALLLNIEKTVCEGAGATGIAAIMSR-----PDL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 IGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKULIEPTAGVALAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Greven C.
APPLICANT: Wiegand, Roger C.
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ISPADVEKAHINIQDSIHLTPVLTSSILNQ-IAGRNLFFKCELFQKTGSFKIRGALNAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%; Score 434; DB 4; 32.8%; Pred. No. 8.1e-39;
                                                                                                                                                                                                       Sequence 12639, Application US/09902540 Patent No. 6833447
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297 RGRRTAIILSGGNIDMNVIS 316
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                                               ---KNVCIVLSGGNVD 318
                                                                                          300 FLGHKVGVVLSGGNID 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Myxococcus xanthus US-09-902-540-12639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 32.8*
Matches 105; Conservative
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                    US-09-902-540-12639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS-- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 --IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EIVLIGDTFDHCLAQALNYTKOHKMN-FIDPFNNVYTIAGOGTLAKEILNQAEKEDKTFD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS-- 124
                                                                                                                                                                                                                                                                                                                                                                              7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic JOTHER INFORMATION: amino acid sequence US-09-710-279-1046
                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                     Query Match 21.0%; Score 365; DB 3; Length 424; Best Local Similarity 29.8%; Pred. No. 3.5e-31; Matches 97; Conservative 60; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.0%; Score 365; DB 4; Length 424; Best Local Similarity 29.8%; Pred. No. 3.5e-31; Matches 97; Conservative 60; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 FOTVSPEVKNVCIVLSGGNVDLTSL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 KKQI--ENKTIVCIVSGGNNDINRM 326
                              60/055,779
                                                                                                                                                                                 ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1046, Application US/09710279 Patent No. 6703492
, PRIOR FILING DATE: 1997-11-08
, PRIOR APPLICATION NUMBER: US 60,
, PRIOR FILING DATE: 1997-08-14
, NUMBER OF SEQ ID NOS: 5674
, LENGTH: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-710-279-1046
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LENGTH: 424
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRNCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
VTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTS 321
                                                                                                               265 YLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIAQH----NIRGERLAHI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS-DESREK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 VTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 KOLMPOIKVIAVE---AEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCOE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAV---LSQHFQTVSPEVKNVCIV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 KALKPSVKVYAAEPSNADD--CYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ::: ||:
32 VYEAVQKTPLQKMDKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMSSL---TAEQKSHG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT.
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-22004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.8%; Score 379; DB 4; Length 521; Best Local Similarity 32.0%; Pred. No. 1.4e-32; Matches 101; Conservative 67; Mismatches 130; Indels
                                                                                                                                                                                                                           322 LNWVGQ------35
                                                                                                                                                                                                                                                                                                                                                                   Sequence 8050, Application US/09489039A
Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 LSGANVNFHGLRYVSE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 LSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8050
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310 IVLSGGNVDLTSLNWVGQAER 330
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: M.catarrhalis
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Best Local Similarity
                                                                                                                                                                                                                          US-09-540-236-3648
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--IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVD 178
                                                           179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                      126 BIVLIGDTFDHCLAQALNYTKQHRAN-FIDPFNNVYTIAGQGTLAKEILNQAEKEDKTFD 184
                                                                               239 GVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ehrlich, Stanislav
APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: Synthase from Lactococcus and its applications
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PSDESREKVTQRIMQETEGILVHPNQEPAVIAGGGTIALEVLNQVP----LVDALVVPVG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 KAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GANIYLKEVUTKTPLQLDPYLSNKYQANIYLKEENLQKVRSFKLRGAYYSISKL--SDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.7%; Score 359.5; DB 1; Best Local Similarity 29.4%; Pred. No. 1.5e.30; Matches 98; Conservative 67; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Lactococcus lactis subsp. lactis INDIVIDUAL ISOLATE: ILVA
                                                                                                                                                                             298 FQTVSPEVKNVCIVLSGGNVDLTSL 322
                                                                                                                                                                                               304 KKQI--ENKTIVCIVSGGNNDINRM 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: GOLDMAN, MICHAEL I.
RESISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 20747/30
TELECHONE: (716) 263-1600
TELEFAX: (716) 263-1487
TELEFAX: (716) 263-1487
                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08403866
Patent No. 5643779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Sequence 3648, Application US/09540236
Fatent No. 6673310
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: NOW DIGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3548
186 GGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSI 244
                                                210 GGGLIAGITAYSKERYPQTEIIGVEAKGATSMKAAYSAGQ-PVTLEHIDKFADGIAVATV 268
                                                                                                   GLNTWPLIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPE 304
                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 HSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASI-VYCDPSDESREKVTQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 RIMOBTEGI-LVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPVGGGGWVAGIAITIKA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 K--AETDGMTYIAPYDDELVIÄGGGTIGLELTQQWRNIDYVFIACGGGLLÄGVAAFLGE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : || | | | | | | | : |
197 VAPHIKVVAVBPEGA-ACLKAALASNKRVRLPQVSLFADGVAVAQIGELPYQIAKLSKSD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 ----DLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 AIH-TPLEPATKLSKKFDNHIRLKREDLÓPVESFKLRGAYNKISGL---SDAQKQKGIIC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 SIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVVT
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                                                                                                                                                                                                   305 V--KNVCIVLSGGNVDLTSLNWVGQAERPAPYQ 335
                                                                                                                                                                                                                                   324 IKGKNIVCIISGGNNDISRMQEI--EERALVYE 354
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Job time : 31.9558 secs
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Sequence 12, Appl Sequence 31, Appl Sequence 31917, A Sequence 27, Appl Sequence 12, Appl Sequence 12, Appl Sequence 20, Appl Sequence 2, Appl Sequence 2, Appl Sequence 6, Appl Sequence 5, Appl Sequence 13876, Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 750, Appl Sequence 750, Appl Sequence 750, Appl Sequence 670, Appl Sequence 17, Appl Sequence 2128, Appl Seque

rotal number

Database

Searched:

Sequence:

Run on:

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61 LNAIRGLIPDTPEEKPKAVVTHSSGNHGQAL,TYAAKLEGIPAYIVVPQTAPNCKKLAIQA
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Publication No. US20020115137A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 340;
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S US-10-424-599-266101
S US-10-424-599-266101
S US-10-425-114-38570
S US-10-425-114-38570
S US-10-425-114-39197
S US-10-425-114-39197
S US-10-413-943-27
S US-10-413-943-12
S US-10-413-943-64
S US-10-413-943-67
S US-10-70-701-378-626-673
S US-10-287-226-673
S US-10-377-072-17
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CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRRESEQ for Windows Version 4.0
    Matches 305; Conservative
    ORGANISM: Homo sapiens
    JS-09-789-300A-2
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LENGTH: 340
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Sequence 2, Appli
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                                                                                                                                                             April 22, 2005, 16:23:43 ; Search time 88.3697 Seconds (without alignments) 1276.639 Million cell updates/sec
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1: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/PCT_PWBCOMB.pep:*} \)

2: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/PCT_BW_PW_PBPpp:*} \)

3: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOF_NEW_PUB.pep:*} \)

4: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOF_NEW_PW_PBP.pep:*} \)

5: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_NEW_PW_PBP.pep:*} \)

6: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_NEW_PW_PBP.pep:*} \)

7: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_NEW_PW_PBP.pep:*} \)

8: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_PWBCOMB.pep:*} \)

9: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_PWBCOMB.pep:*} \)

10: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_PWBCOMB.pep:*} \)

11: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USOB_PWBCOMB.pep:*} \)

13: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

14: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

15: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

16: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

17: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

18: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

19: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

10: \( \text{cgn2} \ \bigcit{6}\) \text{ptodata/1/pubpaa/USIOB_PWBCOMB.pep:*} \)

10: \( \text{cgn2} \bigcit{6}\) \text{ptodata/1/pubpaa/USIO
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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4 US-10-164-966-2
5 US-10-240-866-2
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5 US-10-264-237-2089
5 US-10-437-963-106995
5 US-10-425-114-49567
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180

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Sequence 33, Appl Sequence 29, Appl

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                                LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA
                                                                                                                                             121 YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL
                                                                                                                                                                                                                                  KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                                                                                                                                                             181 VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
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US-10-240-800-2
| Sequence 2, Application US/10240800
| Publication No. US2003021226241
| GENERAL INFORMATION:
| APPLICANT: Merck & Co., Inc.
| TITLE OF INVENTION: HUMAN SERINE RACEMASE
| FILE REFERENCE: 20642Y-PCT
| CURRENT APPLICATION NUMBER: US/10/240,800
| CURRENT FILING DATE: 2002-10-03
| PRIOR APPLICATION NUMBER: 60/194,451
| PRIOR FILING DATE: 2000-04-04
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-240-800-2
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APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INNEWTION: Asacotal E.
TITLE OF INNEWTION: Asacotal Edd Antigen Molecules, Aminotransferase
TITLE OF INNEWTION: Molecules, Armiotransferase
TITLE OF INNEWTION: Molecules, Armiotransferase
TITLE OF INNEWTION: Pyridoxal-Phosphare Dependant Enzyme Molecules,
TITLE OF INNEWTION: Pyridoxal-Phosphare Dependant Enzyme Molecules,
TITLE OF INNEWTION: Pyridoxal-Phosphare Dependant Enzyme Molecules,
TITLE OF INNEWTION: Molecules, Arpase Molecules,
TITLE OF INNEWTION: Therefore
TITLE OF INNEWTION: Molecules, Arpase Molecules,
FILE REFERENCE: 38000-12-20
FRICA FILING DATE: 2000-12-27
FRICA FILING DATE: 2000-11-20
FRICA FILING DATE: 2000-11-30
FRICA FILING DATE: 2000-11-30
FRICA FILING DATE: 2000-11-30
FRICA FILING DATE: 2000-11-30
FRICA FILING DATE: 2001-11-30
FRICA FILING DATE: 2001-01-30
FRICA FILING DATE: 2001-01-
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                                                                                                                                                      121 YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
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                                                                241 KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                           VVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
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                                                                                                                                                                                                                301 VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV 339
                                                                                                                                                                                                                                             301 VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10164966
Publication No. US20030064439Al
GENERAL INFORMATION:
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APPLICANT: Glucksmann Maria
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LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-437-963-106995
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APPLICANT:
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APPLICANT:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
          JOS-10-240-466-2

Sequence 2, Application US/10240466

GENERAL INFORMATION:

APPLICANT: Ramakrishnan, Shyam

TITE OF INVENTION: Regulation of Human Serine Racemase Enzyme

FILE REFERENCE: LIO115-09-30

CURRENT APPLICATION NUMBER: US/10/240,466

CURRENT FILING DATE: 2002-09-30

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR PLICATION NUMBER: US 60/193,748

PRIOR PLING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: US 60/194,249

PRIOR PELING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 340
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Publication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT RAPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: DCT/US01/16450

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

SOFTWARE: PATENTION NUMBER: 13

SOFTWARE: PATENTION NUMBER: 231

SOFTWARE: PATENTION NUMBER: 231

SOFTWARE: PATENTION NUMBER: 231
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89.4%; Pred. No. 9.2e-146;
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Matches 304; Conservative
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                  , LOCATION: (224)
, OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2089
                                                                                                                                                                                                                                 the twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                    56.8%; Score 988; DB 15; Length 2:
89.6%; Pred. No. 3.7e-88;
ive 12; Mismatches 10; Indels
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US-10-437-963-106995
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                                                                                                                                                                NAME/KEY: MISC FEATURE
LOCATION: (210)
OTHER INFORMATION: Xaa equals any of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boukharov, Andrey A.
Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 89.69
Matches 189; Conservative
                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE LOCATION: (224)
Ното варіепв
                                                 NAME/KEY: MISC FEATURE
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ORGANISM: Oryza sativa
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Matches 150; Conserv
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Publication No. US2004003488A1
GENERAL INFORMATION:
Publicant Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Show, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: NOWENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: AND APPLICATION NUMBER: AND APPLICATIO
77 FALDDD----EASKGVVTHSSGNHAAAVALAAKLRGIPAYIVIPRNAPACKVDNVKRYGGH 133
                                                                                                                              125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGGGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                       185 GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSI 244
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                                                                                                                                                                                                                                                                                                                                                           253 GDLTWPVVRDLVDDIIVVDDNAIVDAMKMCYEMLKVAVEPSGAIGLAAALSDEFKQSSAW 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 700335017_FLI.pep
US-10-425-114-49567
                                                                                                                                                                                                                                                                                                                                                                                                                                     304 - EVKNVCIVLSGGNVDLTSLNW 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 HESSKIGIIVSGGNVDLGVL-W 333
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353 HESSKIGIIVSGGNVDLGTL-W 373
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 49567
LENGTH: 379
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Sequence 62761, Application US/10425114

Sequence 62761, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DAPE: 2003-04-28

SEQ ID NOS: 73128

SEQ ID NOS: 73128
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Sequence 155663, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosal Thomas J
APPLICANT: La Rosal Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERENCE: 38-21 (53.23.9)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
IENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 GSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 CKKLAIQAYGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CKVENVKRYGGHIIWSDASIESREYVCKRVQEETGAVLIHPFNSKYTISGQGTVSLLLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 QVPLVDALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNIHP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 PETIADGVKSSIGLNTWPIIRDLVDDVFTVTEDEIKXATQLVWGRMKLLIEPTAGVALAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.8%; Score 640.5; DB 15; Length 280; 46.7%; Pred. No. 5.8e-54; tive 55; Mismatches 84; Indels 7;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_111043C.1.pep
US-10-424-599-155063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3591-097-G1_FLI.pep
US-10-425-114-62761
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Best Local Similarity 46.7%
Matches 128; Conservative
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ORGANISM: Glycine max
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ORGANISM: Zea mays
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us-09-889-609b-8.rapb

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NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Best Local Similarity 37.7'
Matches 118; Conservative
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244 TL-W 246
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SEQ ID NO 43071
                                                                                                                                                                                  180 SEIIKAMKLCFEILKVVVEPSGAIGLAAVLSDTFOK-NPAWKDCNHIGIVVSGGNVDLAM 238
                                                                                                                                                            ETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGNVAGIAITIKALKPSV 204
                                                                                                                                                                                                                                       205 KVYAAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPIIRDLVDDVFTVTE 264
                                                                                                                                                                                                                                                                                                                  DEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSP---EVKNVCIVLSGGNVDLTS 321
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                                                                                                         85 GNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESREKVTQRIMQ
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         Length 247;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9309_1.pep
         33.2%; Score 577; DB 15;
44.9%; Pred. No. 8.1e-48;
tive 58; Mismatches 70
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LOCATION: (1)..(252)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040172684A1
GENERAL INFORMATION:
           Query Match 33.2%,
Best Local Similarity 44.9%,
Matches 109; Conservative
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Matches 104; Conservative
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ORGANISM: Sorghum bicolor
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APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: that Express Feedback Insensitive Threonine Dehydratase/Deaminase
FILE REFERENCE: PRF-07898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 IHGTVVDETLAAAQEYAAETGAVFIHPFDHPDIIAGQGTVGLEILEQCPEVRTIVVGIGG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 DVPFRIIGDLVDEVRTVSEGNLSSALLLCLERAKLVVEPAGASPVAALLREPGAFEGP-- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
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                                                                                                                                                                                                                     APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAKI, YOSHYUKI
APPLICANT: SARAKI, YOSHYUKI
APPLICANT: SARAKI, YOSHYUKI
APPLICANT: SARAKI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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; Sequence 10839, Application US/10156761; Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/10413943 Publication No. US2004006784A1 GENERAL INFORMATION:
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APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: Mat Express Feedback Insensitive Threonine Dehydratase/Deaminase
FILE REPRENCE: PRF-07898
CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
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APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 VTQRIMQETEGILVHPNOEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITI 197
           252 IRDLVDDVFTVTEDBIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV---KNV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 VYEAAQVTPLOKMEKLSSRLDNVILVKREDRÓPVHSFKLRGAYAMMAGL---TEEOKAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||:|||| : ::: |:: ||::||:|| : :||::| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Mismatches 127; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.1%; Score 384; DB 1
32.3%; Pred. No. 2e-28;
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/10413943 Publication No. US20040006784A1 GENERAL INFORMATION:
                                                                                                                                                                                                      364 YVPILSGANMNFDRLRFVSE 383
                                                                                                                                                             309 CI-VLSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Salmonella typhimurium
US-10-413-943-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 LSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 LSGANVNFHGLRYVSE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 32.3%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-266101
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US-10-413-943-31
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US-10-413-943-29
US-10-413-943-29
Sequence 29, Application US/10413943
PUBLICATION NO. US20040006784A1
GENERAL INFORMATION:
APPLICANT: MOUTAGA, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: that Express Peedback Insensitive Threconine Dehydratase/Deaminas
TITLE OF INVENTION: WHOMER: US/10/413,943
CURRENT APPLICATION WUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 IGAYLKRVAPHIKTIGVETYDAATLHNSLQRNQRTP-LPVVGTFADGTSVRMIGEETFRV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVYDVINESPISQGVGLSSRINTNVILKREDLLPVFSFKLRGAYNMIAKL---DDSQRNQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV-YCDPSDESRE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 IGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLS-----Q 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLALQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 PGNLTYEIVRELVDDIVLVSEDEIRNSMIALIQRNKVVTEGAGALACAALLSGKLDQYIQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 -YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
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                                                                                                                                                                                                                                                                                                                                                       7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                      Query Match 27.4%; Score 476; DB 15; I
Best Local Similarity 35.9%; Pred. No. 9.9e-38;
Matches 118; Conservative 70; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 HFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 NRKTVS-----1ISGGNIDLSRVSQI 323
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                                                                   TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                              US-10-413-943-33
SEQ ID NO 33
LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 AITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI------ADGVK-SSI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AAYVKRVKPEVKIFGVEPTDAN------AMALSLHHDQRVILDQVGFADGVAVKEV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 GLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALA---AVLSOHFQTV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 GEETFRICKELIDGVVLVSRDSICASIKDMFEEKRNILEPAGALALAGAEAYCKHH---- 393
                                                                                                                                                                                                                                        17 INIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKP 76
                                                                                                                                                         21.8%; Score 380; DB 15; Length 602;
31.8%; Pred. No. 6.4e-28;
tive 65; Mismatches 118; Indels 38; Gaps
; SEQ ID NO 266101
; LENGTH: 602
; TYPE: PRT
ORGANISM: Glycine max
; PERTURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8230C.1.pep
US-10-424-599-266101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 GVQGKDIVVITSGANMNFDKLRVV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 SPEVIONCIVLSGGNVDLTSLNWV 325
                                                                                                                                                           Query Match 21.8
Best Local Similarity 31.8
Matches 103; Conservative
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Search completed: April 22, 2005, 16:42:20 Job time : 89.3697 secs

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, GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

April 22, 2005, 16:19:29 ; Search time 30.0442 Seconds (without alignments) 844.779 Million cell updates/sec

US-09-889-609B-10 ritle:

Perfect score:

1735 1 MCAQYCISFADVEKAHINIR.....SSITWVKQAERPASYQSVSV 340 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA: Database

1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMAKIES	-	2, Appli	645	4536,		27783,	12639,	5207,			4364,	34, Appl	`.	3876,		3648, 7	10, Appl	7451,	2928,	878,	', Appli	2, Ap	Appli,	, App	.0, Appl	1, Appl:	Appl
	Description	Sequence 2																			Sequence 2	Sequence 1	Sequence 4	Sequence 6	Sequence 1	Sequence 8	Segmence 4
	ID	US-09-789-300A-2	US-09-543-681A-4645	US-09-328-352-4536	US-09-252-991A-31294	US-09-252-991A-27783	US-09-902-540-12639	US-09-328-352-5207	US-09-489-039A-14107	US-09-252-991A-22442	US-09-543-681A-4364	US-09-424-978B-34	US-09-489-039A-8050	US-09-134-001C-3876	US-09-710-279-1046	US-09-540-236-3648	US-08-403-866-10	US-09-328-352-7451	US-09-107-433-2928	US-09-583-110-3878	US-08-669-378-2	US-08-669-378-12	US-08-669-378-4	US-08-669-378-6	US-08-669-378-10	US-08-669-378-8	US-09-789-300A-4
	DB	4	4	4	4	4	4	4	4	4	4	4	4	m	4,	4		4	4	4	m	m	m	m	m	ო	4
de	o Query Match Length	340	332	328	374	524	405	411	334	677	525	507	521	424	424	518	441	520	421	416	436	436	436	436	436	436	378
	Query Match	100.0	34.6	33.3	31.0	26.3	25.6	25.6	25.5	23.2	22.7	21.6	21.3	21.2	21.2	20.5	20.1	19.9	19.4	19.0	17.9	17.9	17.8	17.8	17.8	17.7	16.3
	Score	1735	601	578	538	457	445	443.5	442	403	393	375	369	367	367	355	348.5	344.5	336	330	310.5	310.5	309.5	309.5	309.5	307.5	283 5
	Result No.	-	7	м	4	Ŋ	9	7	σ,	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26

Sequence 10697, A Sequence 6763, Ap	Sequence 1, Appli Sequence 29393, A	Sequence 18227, A Sequence 4168, Ap	Sequence 29, Appl Sequence 18228, A		Sequence 4532, Ap	Sequence 3925, Ap	Sequence 17694, A	Sequence 3983, Ap	Sequence 5, Appli	Sequence 161, App	Sequence 1075, Ap	Sequence 2, Appli	Sequence 9, Appli
US-09-949-016-10697 US-09-949-016-6763	US-09-088-435-1 US-09-252-991A-29393	US-09-248-796A-18227 US-09-134-001C-4168	US-09-424-978B-29 US-09-248-796A-18228	US-09-583-110-4369	US-09-107-433-4532	US-09-107-532A-3925	US-09-248-796A-17694	US-09-134-000C-3983	US-09-962-357-5	US-08-311-731A-161	US-09-538-092-1075	US-08-120-960-2	US-09-347-878-9
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274.5 265.5	259.5 256	242.5 241.5	237	196.5	196.5	195	193.5	191	190.5	187	187	187	187
28 29	30 31	32 33	34 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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61 LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIFAYIVVPQTAPDCKKCAIQA 120
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            Sequence 2, Application US/09789300A
Patent No. 6458576
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR PILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 340
TYPE: PRT
US-09-789-300A-2
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301 VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340

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Sequence 31294, Application US/09252991A
Patent No. 651795
GENERAL INFORMATION
TERMINATION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AFRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AFRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/0/074,788
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER: US/0/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                  68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
                                                                          GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IGL 246
                                                                                                                                                                                                                  247 NTWPLIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV- 305
                                                                                                                                                                                                                                                                                   250 LTFPIIQQKVDDILITYIDEELINAMKFFABRNKOVVEPIGCLGFAAA----RNLKDELK 304
 68 VPDALERKFKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
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37.7%; Pred. No. 2.5e-52;
Live 67; Mismatches 120; Indels
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Best Local Similarity 37.7%
Matches 118; Conservative
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353 RVGILLSGGNIDL 365
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US-09-252-991A-31294
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US-09-252-991A-31294
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                               Sequence 4645, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION WUMBER: US/09/543,681A
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUDANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
WUMBER OF SEQ ID NOS: 8252
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Patent No. 6562958
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Proteus mirabilis
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RESULT 2
US-09-543-681A-4645
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LENGTH: 328
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US-09-902-540-12639
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SEQ ID NO 12639
LENGTH: 405
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                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27783

LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-27783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 NHAQGLALAAXRQGIRAVIVMPKTTPEIKVQAVRAHGAKAVLHGDAFPEALAHALKLV-D 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETEGIMVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMLAGIAITVKALKPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 TEDEIKCATOLVWERMKLLIEPTAGVGVAAVLSOHFOTVSPEVKNICIVLSGGNVDL--- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegard, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 VKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.3%; Score 457; DB 4; Length 524; ilarity 35.2%; Pred. No. 7.8e-43; Conservative 63; Mismatches 127; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 RHVAERAELGERREAİIAVTIPERPGSFKA 364
                                                                        Sequence 27783, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
8.09-902-540-12639
; Sequence 12639, Application US/09902540
; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 GGGGLISGIACALKETRPDIRVVGVQAETIASMKASVEAGERVLLAAAGTrIADGIAVKR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV--- 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GGGMLAGIAITVKALKPSVKVYAAE----PSNADDCYQSKLKGKLMPN----LYPPETIA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTG-RNLFFKCELFQKTGSFKIRGALNAVR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 DIHAAARRLDGLVVKTPFVPSETISKTLGAKOMLKFBNLQFTASFKERGALNKLLSL--- 71
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                                                                                                                                                                                                                                                       Length 405;
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                                                                                                                                                                                                                                          Query Match 25.6%; Score 445; DB 4; Length 40 Best Local Similarity 33.9%; Pred. No. 1.2e-41; Matches 107; Conservative 66; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5207, Application US/09328352 Patent No. 6562958
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US-09-328-352-5207
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297 RGRRTAIILSGGNIDM 312
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TYPE: PRT ORGANISM: Myxococcus xanthus
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UDGANOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US(99/543,681A
FILE REPERENCE: 2000-04-05
FILE REPERENCE: 2000-04-05
FILE REPERENCE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4364
ILENGTH: 525
                                                                                                                                                                                                                                             194 TPLOVAPQLSORLGNRVLLKREDLOPVFSFKIRGAYTRVARL---SDEOKARGVITASAG 250
                                                                                                                                                                                                                                                                             86 NHGQALIYAAKLEGIPAXIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRV-TE 144
                                                                                                                                                                                                                                                                                                   SVKVYAAREPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 VTEDRIKCATOLVWERMKLLIBPTAGVGVAAVLSQHPQTVSPEVKNICIVLSGGNVDL-- 319
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369 DIRVIGVEPEDS-NCLQAALAAGERVVLGQVGLFADGVAVAQIGACNFEVCKDHVDEVIT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGA-S 124
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                                                                                                                                                                                                              26 TPVLISSILNQLIGRNLFFKCELPOKTGSFKIRGALNAVRSLVBDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                145 ETEGI-MYHPNQEPAVIAGOGTIALEVLNQ-VPLVDALVVPVGGGGMLAGIAITVKALKP
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV
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                                                                                                                                                23.2%; Score 403; DB 4; Length 677
33.5%; Pred. No. 1.8e-36;
.ive 60; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.7%; Score 393; DB 4; Length 525; 33.0%; Pred. No. 1.6e-35; ive 67; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TSSITWVKQAERPASYQS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 LRHVAERAELGEQREAIIAVTVAERPGSFKA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4364, Application US/09543681A
Patent No. 6605709
                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                           Best Local Similarity 33.59
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.7;
Best Local Similarity 33.0°
Matches 104; Conservative
                       ; NUMBER OF SEQ ID NOS:
; SEQ ID NO 22442
; LENGTH: 677
                                                                                                          US-09-252-991A-22442
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US-09-543-681A-4364
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REPERENCE: 2709.2004.01
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22442, Application US/09252991A
Sequence 22442, Application US/09252991A
Patent No. 6551795
GENERAL INPROMATION:
PAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
CURRENT APPLICATION NUMBER: US/092.25,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
DGVK-SSIGLNTWPIIRDLVDDIFTVTEDBIKCATQLVWERNKLLIEPTAGVGVAAVLSQ 296
                     67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 YCEPSDESRENVAKR--VTEFTEGIMVHPNQEPAVIAGGGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 L--HGDNFNDTLAKASDIVELEGRIFIPPYDDPQVIAGGGTIGLEILEDLYDVDNVIVPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 IGLNIWPIIRDLVDDIFTVTEDBIKCATQLVWBRMKLLIEPTAGVGVAAVLS-----Q 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 442; DB 4; Length 334;
; Pred. No. 1.9e-41;
66; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 HFQTVSPEVKNICIVLSGGNVDLT--SSIT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.5%; Score 442; 34.8%; Pred. No. 1
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-----PDLFLGHKVGVVLSGGNID 315
                                                                 297 HFQTVSPEV---KNICIVLSGGNVD 318
                                                                                                                                                                                   Sequence 14107, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 115; Conserv
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US-09-252-991A-22442
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us-09-889-609b-10.rai

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Matches 100;
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ORGANISM:
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244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 DALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 DALAR---GVITASAGNHAQGVAFSAARMGVKAVIVVPVTTPQVKVDAVRAHGGPGVEVI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 PSDESRENV---AKRVTEETEGIMVHPNQEPAVIAGGGTIALEVL--NQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 QAGESYSDAYAHALKVQEERGLTFVHPFDDPYVIAGQGTIAMEILRQHQGP-IHAIFVPI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 HLTPVLTSSILNQL-----TGRNL-----FFKCELFQKTGSFKIRGALNAVRSLVP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kinney, Anthony J.
APPLICANT: Abell, Lynne N.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: BB-1087
CURRENT APPLICATION NUMBER: US/09/424,978B
CURRENT FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/048,771
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 34
LENGTH: 507
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; Sequence 8050, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                    Sequence 34, Application US/09424978B Patent No. 6664445
                                                                                                                                                                                                                                                                                     APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Scephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hitz, William D.
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ORGANISM: Burkholderia capacia
                                                                                                                    304 EVKNICIVLSGGNVD 318
                                                                                                                                        307 KGERLAHVLSGANVN 321
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Matches 105; Conservative
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Sequence 3876, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION:
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
     NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 AIELAQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHIDRVFVVGGGGLAAGVAVLIK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 ALKPSVKVYAAEPSNADD--CYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDL 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                              PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUT
                                                                                                                                                                                                                                                                                                                                                                                  Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 369; DB 4; 31.7%; Pred. No. 8.6e-33;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO A; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTI; FILE REFERENCE: 2709,2004001; CURRENT APPLICATION NUMBER: US/09/489,039A; CURRENT FILING DATE: 2000-01-27; PRIOR FILING DATE: 1999-01-29; NUMBER OF SEQ ID NOS: 14342
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Best Local Similarity 31.78
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Best Local Similarity
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US-09-134-001C-3876
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125 -IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNOV----PLVDA 179
                                                                                       67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS-- 124
                                                                                                                                 180 LVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG 239
                                                                                                                                                      240 VK-SSIGLNTWPIIRDLVDDIFTVTEDBIKCATQL-VWERMKLLIEPTAGVGVAAVLSQH 297
                                                                                                                                                                                                                          246 ASVARVGDITFDIAKDKVDDYVQVDEGAV-CSTILDMYSKQAIVAEPAGALSVSA-LEQY 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 -IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNOV----PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKIKGKLMPNLYPPETIADG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: STREPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 L---SNEKKNKGITCASAGNHAQGVAYTAKKLNLKAVIEMPVTFPRQKINQVKFFGDSNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.2%; Score 367; DB 4; Length 424;
Best Local Similarity 31.1%; Pred. No. 1e-32;
Matches 100; Conservative 64; Mismatches 142; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                   298 FQTVSPEVKNICIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                           304 KKQI--ENKTIVCIVSGGNNDI 323
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; Sequence 1046, Application US/09710279
; Patent No. 6703492
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ORGANISM: Artificial Sequence
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RESULT 15

US-09-540-236-3648

US-09-540-236-3648

Sequence 3649, Application US/09540236

RECENT NO. 6673910

GENERAL INFORMATION:

APPLICANT: GETY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF

FILE REPERBNCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

WUMBER OF SEQ ID NOS: 3840

LENGTH: 518
                                                                                                                                                                                                                                                                                                                                                                                                                                 82 HSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASI-VYCEPSDESRENVAK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 RVTEETEGI-MVHPNQEPAVIAGQGTIALEVINQVPLVDALVVPVGGGGMLAGIAITVKA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVT 81
                                                                                                                                                                                                                                                                                                                                                                                           ----DLVDDIFTVTEDBIKCATQLVWERMKLLIEPTAGVGVAAVLSOHFQTVSPEVKNIC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 GSGTVIEPEIVTCTNDEICAAIKDIFEENRSIVE-TAGALSVAGMKKFIQTHNLSGKNCV 314
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                                                                                                                                                                                                                                                                                                     20.5%; Score 355; DB 4; Length 518; 32.4%; Pred. No. 3.4e-31; ive 63; Mismatches 126; Indels
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                                                                                                                                                                                                                                                                                                                 Local Similarity 32.4
nes 100; Conservative
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: M.catarrhalis
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US-09-540-236-3648
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Matches
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LENGTH: 340
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Sequence 106995,
Sequence 49567, A
Sequence 62761, A
Sequence 43071, A
Sequence 10839, A
Sequence 33, Appl
Sequence 33, Appl
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Sequence 2, Appli
Sequence 2, Appli
                                                                                                                            April 22, 2005, 16:23:43 ; Search time 88.6303 Seconds (without alignments) 1276.639 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/PCT_NEW PUB.COMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/NGG NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USOG NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USOG NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOB PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-240-800-2
US-10-240-466-2
US-10-240-466-2
US-10-264-237-2089
US-10-427-963-106995
US-10-425-114-49567
US-10-424-599-155063
US-10-424-599-155063
US-10-156-701-10839
US-10-156-71-10839
US-10-413-943-33
US-10-425-114-39197
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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ALIGNMENTS

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61 INAVRSLVPDALERKPKAVVTHSSGNHGQALTYAARKLEGIPAYIVVPQTAPDCKKLAIQA 120
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                                                                                                        APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35809/208926
FILE REFERENCE: 35809/208926
CURRENT APPLICATION NUMBER: US/09/789, 300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183, 208
PRIOR APPLICATION NUMBER: US 60/183, 208
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 2, Application US/09789300A Publication No. US20020115137A1 GENERAL INFORMATION:
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                                    LNAVRSLVPDALERKPKAVVTHSSGNHGQALITYAAKLEGIPAYIVVPQTAPDCKKLAIQA
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                                                                                                                                           181 VVPVGGGMLAGIAITVKALKPSVKVYAABPSNADDCYQSKLKGKLMPNLYPPETIADGV
                                                                                                                                                        61 LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA
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100.0%; Pred. No. 2.4e-162;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          Sequence 2. Application US/10240800
Publication No. US20030212262A1
GENERAL INPORMATION:
TITLE OF INVENTION: HUMAN SERINE RACEMASE
FILE REFERENCE: 20642Y-PCT
CURRENT PELING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 340; Conservative
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US-10-240-800-2
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LENGTH: 340
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                                                            KSSIGINTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGYGVAAVLSQHFQT 300
                                                                         241 KSSIGLNTWPIIRBLVDDIFTVTEDEIKCATQLVWERMKLLIEFTAGVGVAAVLSGHFGT 300
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                     VVPVGGGGMLAGIALTVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
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100.0%; Score 1735; DB 14; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.4e-162;
Matches 340; Conservative 0; Mismatches 0; Indels 0;
                                                                                                   VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                               US-10-164-966-2; Sequence 2, Application US/10164966; Publication No. US20030064439A1; GENERAL INFORMATION:
                                                                                                                                                                                                     APPLICANT: Bandaru, Rajasehkar
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LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                   APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human Serine Racemase Enzyme
FILE REFERENCE: L10115-US
CURRENT PILIORS DATE: 2002-09-30
PRIOR FILING DATE: 2002-09-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR PRICATION NUMBER: US 60/193,748
PRIOR PELICATION NUMBER: US 60/193,748
PRIOR PELICATION NUMBER: US 60/194,249
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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Bublication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA111P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: DCS-18

PRIOR FILING DATE: 2001-05-18

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PATENTIN Ver. 3.1

LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
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                                  Sequence 2, Application US/10240466 Publication No. US20030175941A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-264-237-2089
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 340
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Associated With
                                                                                                            OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 RSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 106995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VVPVGGGGMLAGIAITVKALKPSVKVYAXXP-QMQMTVPVQAEGXLMP 227
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Pred. No. 3.3e-96;
2; Mismatches 12; Indels
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US-10-437-963-106995
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47.1%; Pred. No. 1.8e-67;
itive 64; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106995, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 93.4%;
Matches 213; Conservative
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                                                                                                                                   FEATURE:
NAME/KEY: MISC_FEATURE
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (224)
ORGANISM: Homo sapiens
                                                       NAME/KEY: MISC_FEATURE
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Best Local Similarity
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) OTHER INFORMATION: Clone ID: LIB3591-097-G1_FLI.pep
US-10-425-114-62761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ALSDEFKQSSAWHESSKIGIIVSGGNVDL 270
                                                                 Sequence 62761, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
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Best Local Si
Matches 128;
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Soreen, Steven E

APPLICANT: Go, Yorgwei

APPLICANT: Go, Yorgwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 49567
125 IVYCEPSDESRENVAKRYTEFTEGIMVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
                                                            |:: : | ||||:||||| ||| |:|||
134 IIWSDVSIESRESVAKRVQEETGAILVHPFNNKNTISGQGTVSLELLEEVPEIDTIIVPI 193
                                                                                                                  185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSI 244
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253 GDLTWPUVRDLVDDIIVVDDNAIVDAMKMCYEMLKVAVEPSGAIGLAAALSDEFKQSSAM 312
                                                                                                                                                        245 GLNTWPIIRDLVDDIFTVTEDBIKCATOLVWERMKLLIEPTAGVGVAAVLSOHFOTVSP- 303
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117 FALDD---EQVSKGVVTHSSGNHAAAVALAAKLRGIPAHIVIPRNAPACKVENVKRYGGH 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.5%; Score 755; DB 15; Length 379;
46.1%; Pred. No. 1.6e-65;
tive 66; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 700335017_FLI.pep
US-10-425-114-49567
                                                                                                                                                                                                             304 -EVKNICIVLSGGNVDLTSSITW 325
                                                                                                                                                                                                                                  313 HESSKIGIIVSGGNVDL--GVLW 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 -EVKNICIVLSGGNVDL 319
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Best Local Similarity 46.1%
Matches 146; Conservative
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                                                                                                                                                                                                                                                                                              -10-425-114-49567
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Sequence 155063, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: About to David K
APPLICANT: Story APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cor, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62761
LENGTH: 280 53 GSFKIRGALNAVRSIVPDALERKPKAVVTHSSGNHGGALTYAAKLEGIPAYIVVPOTAPD 112 113 CKKLAIQAYGASIVYCEPŞDEŞRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLN 172 173 GVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYP 232 233 PETIADGVKSSIGLNTWPIIRDIVDDIFTVTEDEIKCATOLVWERNKLLIEPTAGVGVAA 292 |:||||||||:::| 6 GAFKIRGASNSIFALDD---EQVSKGVVTHSSGNHAAAVALAAKLRGIFAHIVIPRNAPA 62 9 37.5%; Score 651; DB 15; Length 280; 47.6%; Pred. No. 1.9e-55; tive 56; Mismatches 79; Indels ; ; OTHER INFORMATION: Clone ID: PAT_MRT3847_111043C.1.pep US-10-424-599-155063 FEATURE:

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APPLICANT: Mourad, George S, TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms FITLE OF INVENTION: That Express Peedback Insensitive Threonine Dehydratase/Deaminase CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 GGGLAAGIATAVKALRPDVRIVGVQAAGA-AAYPPSLAAGRPVSVENPATMADGIKVGRP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASI- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 VYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
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37.9%; Pred. No. 2.8e-38;
tive 53; Mismatches 131; Indels
                                                                                                                                                                                                                                    APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
SEQ ID NO 10839
                           Sequence 10839, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptomyces avermitilis
US-10-156-761-10839
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; Sequence 33, Application US/10413943
; Publication No. US20040006784A1
; GENERAL INFORMATION:
                                                                                                                                   IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 37.94
Matches 119; Conservative
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                                                                                                           APPLICANT: OMURA, SATOSHI
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APPLICANT:
APPLICANT:
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 43071
                                                                                                                                                                                                                                               180 SEIIKAMKLCFEILKVVVEPSGAIGLAAVLSDTFOK-NPAWKDCNHIGIVVSGGNVDL-- 236
                                                                                                             85 GNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTE 144
                                                                                                                                                                                                                ETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSV 204
                                                                                                                                                                                                                                                                                                                      205 KVYAAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPIIRDLVDDIFTVTE 264
                                                                                                                                                                                                                                                                                                                                                                       121 RIFAAEPKGADDAAQSKAAGRII-RLPETNTIADGLRAFLGDFTWPVVRDLVEEIITVED 179
                                                                                                                                                                                                                                                                                                                                                                                                                              DEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP---EVKNICIVLSGGNVDLTS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 SGNHGQALIYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 VKVYAAEPSN-ADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPIIRDLVDDIFTV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                         7;
        DB 15; Length 247;
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43.9%; Pred. No. 3.4e-42;
Live 48; Mismatches 82; Indels
                                                         65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9309_1.pep
Query Match
34.0%; Score 590.5; DB 1.
Best Local Similarity 46.3%; Pred. No. 1.4e-49;
Matches 113; Conservative 59; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (1)..(252)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43071, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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Best Local Similarity 43.9%
Matches 105; Conservative
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ORGANISM: Sorghum bicolor
FEATURE:
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237 AMLW 240
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Publication 05/10413943
Publication 05/10413943
Publication No US20040006784A1
Publication No US20040006784A1
APPLICAMT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: That EXpress Feedback Insensitive Threonine Dehydratase/Deaminase
FILE REFERENCE: PRP-07898
CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
                                                                                                                                                                                                                                                                             APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: To screen, Steven E
APPLICANT: To screen, Steven E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313) B
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 55647
                       70 DALBRKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |::|||| || ::| ||| ::|
185 GLIAGIAAYVKRVRPEVKIIGVEPSDANAMALSLYHGKRV-MLEHVGGFADGVAVKAVGE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 NTWPLIRDLVDDIFTVTEDBIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 HLTPVLTSSI-----LNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 TEDEIKCATOLVWERMKLLIEPTAGVGVAAVLSQHPQTVSPEVKNICIVLSGGNVD 318
                                                                                                         130 PSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.3%; Score 387.5; DB 15; 32.4%; Pred. No. 4.8e-29; tive 65; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 700478009_FLI.pep US-10-425-114-55647
                                                                                                                                                                                                                      ; Sequence 55647, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 32.4
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 NICIVLSGGNVD 318
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APPLICANT: Schou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Number: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
                                                                                                                                                                                               67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
                                                                                                                                                                                                                          184 VGGCGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-S 242
                                                                                                                                                                                                                                                                          127 YCEPSDESRENVAKRVTE--ETEG-IMVHPNQEPAVIAGOGTIALGVINQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                                               243 SIGLNIWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLS----- 295
                                                                                                                                            242 RPGNLTYELVRELVDDIVLVSEDEIRNSMIALIQRNKVVTEGAGALACAALLSGKLDQYI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 TEGIMVHPNQEPAVIAGGGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 VKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFTV 262
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                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
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                                 Query Match

26.3%; Score 457; DB 15; Length 329;
Best Local Similarity 36.6%; Pred. No. 3.4e-36;
Matches 121; Conservative 65; Mismatches 117; Indels 2
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| ONRKTVS-----11SGGNIDLSRVSQIT 324
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US-10-425-114-39197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39197, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
US-10-413-943-33
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78 AVVITHSSGNHGQALIYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV-YCEPSDESRE 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 GAYLKRVAPHIKTIGVETYDAATLHNSLQRNQRTP-LPVVGTFADGTSVRMIGEETFRVA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 QQVVDEVVLVNTDEICAAVKDIFEDTRSIVEPSGALSVAG-MKKYISTVHPEIDHTKNTY 364
                                                                                                                                                                                                                                   18 NIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPK 77
                                                                                                                                                          Query Match
22.3%; Score 387.5; DB 15; Length 576;
Best Local Similarity 33.9%; Pred. No. 5.7e-29;
Matches 105; Conservative 59; Mismatches 131; Indels 15; Gaps
                                                                           TYPE: PRT;
; ORGANISM: Saccharomyces cerevisiae
US-10-413-943-29
NUMBER OF SEQ ID NOS: 69
SOFWARE: Patentin version 3.2
SEQ ID NO 29
LENGTH: 576
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